CtR 44
handwritten top right

CRF Errors Corrected by the STIC Systems Branch

Serial Number: O8/113,561

CRF Processing Date: 9/7/93
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

ENTERED

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Inserted a space between the last nucleic designator and the nucleic number for sequences:

_____

☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Other:

_____

_____

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

8/01/93

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/113,561

DATE: 09/07/93
TIME: 15:21:27

INPUT SET: S1444.raw

SEQUENCE LISTING

1
2
3 (1)   General Information:
4
5   (i) APPLICANTS: Adams, Thomas R. et al.
6
7   (ii) TITLE OF INVENTION: Methods and Compositions for the
8   Production of Stably Transformed, Fertile, Monocot Plants
9   and Cells Thereof
10
11 (iii) NUMBER OF SEQUENCES: 13
12
13   (iv) CORRESPONDENCE ADDRESS:
14   (A) ADDRESSEE: Arnold, White & Durkee
15   (B) STREET: P.O. BOX 4433
16   (C) CITY: Houston
17   (D) STATE: TX
18   (E) COUNTRY: USA
19   (F) ZIP: 77210
20
21   (v) COMPUTER READABLE FORM:
22   (A) MEDIUM TYPE: Floppy disk
23   (B) COMPUTER: IBM PC compatible
24   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25   (D) SOFTWARE: Patent In Release #1.0, Version #1.25
26
27   (vi) CURRENT APPLICATION DATA:
28   (A) APPLICATION NUMBER: unknown
29   (B) FILING DATE: August 25, 1993
30   (C) CLASSIFICATION: unknown
31
32 (viii) ATTORNEY/AGENT INFORMATION:
33   (A) NAME: Parker, David L.
34   (B) REGISTRATION NUMBER: 32,165
35   (C) REFERENCE/DOCKET NUMBER: DEKA:055/PAR
36
37   (ix) TELECOMMUNICATION INFORMATION:
38   (A) TELEPHONE: 512-320-7200
39   (B) TELEFAX: 512-474-7577
40   (C) TELEX: NOT APPLICABLE
41
42
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45   (i) SEQUENCE CHARACTERISTICS:
46   (A) LENGTH: 15 amino acid residues
47   (B) TYPE: amino acid
48   (C) STRANDEDNESS: single
49   (D) TOPOLOGY: linear
50
51   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

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INPUT SET: S1444.raw

```
 52
 53    Met Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp
 54     1               5                  10                  15
 55
 56
 57    (2) INFORMATION FOR SEQ ID NO:2:
 58
 59       (i) SEQUENCE CHARACTERISTICS:
 60            (A) LENGTH: 35 base pairs
 61            (B) TYPE: nucleic acid
 62            (C) STRANDEDNESS: single
 63            (D) TOPOLOGY: linear
 64
 65       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 66
 67    GAGGATCCGT CGACATGGTA AGCTTAGCGG GCCCC                          35
 68
 69
 70    (2)    INFORMATION FOR SEQ ID NO:3:
 71
 72       (i) SEQUENCE CHARACTERISTICS:
 73            (A) LENGTH: 29 base pairs
 74            (B) TYPE: nucleic acid
 75            (C) STRANDEDNESS: single
 76            (D) TOPOLOGY: linear
 77
 78       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 79
 80    GATCCGTCGA CCATGGCGCT TCAAGCTTC  29
 81
 82
 83    (2) INFORMATION FOR SEQ ID NO:4:
 84
 85       (i) SEQUENCE CHARACTERISTICS:
 86            (A) LENGTH: 29 base pairs
 87            (B) TYPE: nucleic acid
 88            (C) STRANDEDNESS: single
 89            (D) TOPOLOGY: linear
 90
 91       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 92
 93    GCAGCTGGTA CCGCGAAGTT CGAAGGGCT    29
 94
 95
 96
 97    (2) INFORMATION FOR SEQ ID NO:5:
 98
 99       (i) SEQUENCE CHARACTERISTICS:
100            (A) LENGTH: 49 base pairs
101            (B) TYPE: nucleic acid
102            (C) STRANDEDNESS: single
```

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RAW SEQUENCE LISTING
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INPUT SET: S1444.raw

```
103                  (D)  TOPOLOGY: linear
104
105          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:5:
106
107     CTAGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC     49
108
109
110     (2)  INFORMATION FOR SEQ ID NO:6:
111
112          (i)  SEQUENCE CHARACTERISTICS:
113                  (A)  LENGTH: 49 base pairs
114                  (B)  TYPE: nucleic acid
115                  (C)  STRANDEDNESS: single
116                  (D)  TOPOLOGY: linear
117
118          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:6:
119
120     CCGGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTTGT      49
121
122
123
124     (2)  INFORMATION FOR SEQ ID NO:7:
125
126          (i)  SEQUENCE CHARACTERISTICS:
127                  (A)  LENGTH: 11 amino acid residues
128                  (B)  TYPE: amino acid
129                  (C)  STRANDEDNESS: single
130                  (D)  TOPOLOGY: linear
131
132          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:7:
133
134     Met Ala Ser Met Gln Gly Leu Met His Pro Gly
135      1               5                   10
136
137
138     (2)  INFORMATION FOR SEQ ID NO:8:
139
140          (i)  SEQUENCE CHARACTERISTICS:
141                  (A)  LENGTH: 6 amino acid residues
142                  (B)  TYPE: amino acid
143                  (C)  STRANDEDNESS: single
144                  (D)  TOPOLOGY: linear
145
146          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:8:
147
148     Val Lys Cys Met Gln Val
149      1               5
150
151
152     (2)  INFORMATION FOR SEQ ID NO:9:
153
```

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

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INPUT SET: S1444.raw

```
154          (i)  SEQUENCE CHARACTERISTICS:
155               (A)  LENGTH: 18 base pairs
156               (B)  TYPE: nucleic acid
157               (C)  STRANDEDNESS: single
158               (D)  TOPOLOGY: linear
159
160          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
161
162  AAGUGAAGUG AAGUGAAG     18
163
164
165
166  (2) INFORMATION FOR SEQ ID NO:10:
167
168          (i)  SEQUENCE CHARACTERISTICS:
169               (A)  LENGTH: 1845 base pairs
170               (B)  TYPE: nucleic acid
171               (C)  STRANDEDNESS: single
172               (D)  TOPOLOGY: linear
173
174          (ii) MOLECULE TYPE: DNA (genomic)
175
176          (ix) FEATURE:
177               (A)  NAME/KEY: CDS
178               (B)  LOCATION: 1..1839
179
180          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
181
182  ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC   48
183  Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
184   1               5                  10                  15
185
186  AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT   96
187  Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
188           20                  25                  30
189
190  TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC  144
191  Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
192           35                  40                  45
193
194  GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC  192
195  Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
196           50                  55                  60
197
198  TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT  240
199  Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
200   65                  70                  75                  80
201
202  GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC  288
203  Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
204           85                  90                  95
```

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205
206   ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA   336
207   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
208           100                 105                 110
209
210   TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA   384
211   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
212           115                 120                 125
213
214   GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT   432
215   Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
216       130                 135                 140
217
218   ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG   480
219   Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
220   145                 150                 155                 160
221
222   TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC   528
223   Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
224                   165                 170                 175
225
226   GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC   576
227   Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
228                   180                 185                 190
229
230   TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG   624
231   Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
232           195                 200                 205
233
234   CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC   672
235   Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
236       210                 215                 220
237
238   GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG   720
239   Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
240   225                 230                 235                 240
241
242   CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA   768
243   Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
244                   245                 250                 255
245
246   ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG   816
247   Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
248                   260                 265                 270
249
250   CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA   864
251   Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
252           275                 280                 285
253
254   CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC   912
255   Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
```

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256        290                    295                    300
257
258    ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA    960
259    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
260    305                    310                    315                    320
261
262    ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA    1008
263    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
264                325                    330                    335
265
266    CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT    1056
267    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
268                340                    345                    350
269
270    CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC    1104
271    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
272                355                    360                    365
273
274    CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC    1152
275    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
276                370                    375                    380
277
278    GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA    1200
279    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
280    385                    390                    395                    400
281
282    TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG    1248
283    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
284                405                    410                    415
285
286    AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT    1296
287    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
288                420                    425                    430
289
290    GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC    1344
291    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
292                435                    440                    445
293
294    CGC GCT CCT ATG TTC TCC TGG ATC CAT CGC AGC GCT GAA TTT AAC AAC    1392
295    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
296    450                    455                    460
297
298    ATC ATT GCC TCC GAT AGC ATT ACC CAA ATC CCT GCC GTG AAG GGC AAC    1440
299    Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
300    465                    470                    475                    480
301
302    TTT CTG TTT AAT GGT TCC GTG ATT TCC GGC CCA GGC TTT ACC GGT GGC    1488
303    Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
304                485                    490                    495
305
306    GAC CTG GTG CGC CTG AAT AGC AGC GGC AAT AAC ATT CAG AAT CGC GGC    1536
```

```
307    Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
308            500             505             510
309
310    TAC ATT GAA GTG CCA ATT CAC TTC CCA TCC ACC TCC ACC CGC TAC CGC    1584
311    Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
312            515             520             525
313
314    GTG CGC GTG CGC TAC GCT TCC GTG ACC CCA ATT CAC CTC AAC GTT AAC    1632
315    Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
316        530             535             540
317
318    TGG GGC AAT TCC TCC ATT TTT TCC AAT ACC GTG CCA GCT ACC GCT ACC    1680
319    Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
320    545             550             555             560
321
322    TCC CTG GAT AAT CTG CAA TCC AGC GAT TTT GGT TAC TTT GAA AGC GCC    1728
323    Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
324            565             570             575
325
326    AAT GCT TTT ACC TCC TCC CTG GGT AAT ATC GTG GGT GTG CGC AAT TTT    1776
327    Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
328            580             585             590
329
330    AGC GGC ACC GCC GGC GTG ATC ATC GAC CGC TTT GAA TTT ATT CCA GTG    1824
331    Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
332            595             600             605
333
334    ACC GCC ACC CTC GAG TAGGTA                                         1845
335    Thr Ala Thr Leu Glu
336        610
337
338    (2) INFORMATION FOR SEQ ID NO:11:
339
340        (i) SEQUENCE CHARACTERISTICS:
341            (A) LENGTH: 613 amino acids
342            (B) TYPE: amino acid
343            (D) TOPOLOGY: linear
344
345        (ii) MOLECULE TYPE: protein
346
347        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
348
349    Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
350     1               5               10              15
351
352    Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
353            20              25              30
354
355    Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
356        35              40              45
357
```

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

DATE: 09/07/93
TIME: 15:21:52

INPUT SET: S1444.raw

```
358   Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
359        50              55              60
360
361   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
362    65              70              75                  80
363
364   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
365                85              90                  95
366
367   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
368            100             105             110
369
370   Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
371        115             120             125
372
373   Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
374        130             135             140
375
376   Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
377   145             150             155             160
378
379   Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
380            165             170             175
381
382   Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
383            180             185             190
384
385   Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
386        195             200             205
387
388   Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
389        210             215             220
390
391   Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
392   225             230             235             240
393
394   Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
395            245             250             255
396
397   Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
398            260             265             270
399
400   Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
401        275             280             285
402
403   Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
404        290             295             300
405
406   Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
407   305             310             315             320
408
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

```
409    Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
410                    325                 330                 335
411
412    Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
413                340             345                 350
414
415    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
416            355             360                 365
417
418    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
419        370             375                 380
420
421    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
422    385             390                 395                 400
423
424    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
425                405                 410                 415
426
427    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
428                420                 425                 430
429
430    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
431            435                 440                 445
432
433    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
434        450             455                 460
435
436    Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
437    465                 470                 475                 480
438
439    Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
440                485                 490                 495
441
442    Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly
443            500             505                 510
444
445    Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
446            515             520                 525
447
448    Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
449        530             535                 540
450
451    Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
452    545             550                 555                 560
453
454    Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
455                565                 570                 575
456
457    Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
458                580                 585                 590
459
```

```
460   Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
461            595                 600                 605
462
463   Thr Ala Thr Leu Glu
464            610
465
466   (2) INFORMATION FOR SEQ ID NO:12:
467
468          (i) SEQUENCE CHARACTERISTICS:
469                (A) LENGTH: 1848 base pairs
470                (B) TYPE: nucleic acid
471                (C) STRANDEDNESS: single
472                (D) TOPOLOGY: linear
473
474          (ii) MOLECULE TYPE: DNA (genomic)
475
476          (ix) FEATURE:
477                (A) NAME/KEY: CDS
478                (B) LOCATION: 1..1842
479
480          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
481
482   ATG GAT AAC AAT CCG AAC ATC AAT GAA TGC ATT CCT TAC AAT TGC CTC      48
483   Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
484    1               5                  10                  15
485
486   AGC AAC CCT GAA GTG GAA GTG CTG GGT GGC GAA CGC ATC GAA ACC GGT      96
487   Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
488            20                 25                  30
489
490   TAC ACC CCA ATC GAT ATT TCC CTG TCC CTG ACC CAA TTT CTG CTG AGC     144
491   Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
492            35                 40                  45
493
494   GAA TTT GTG CCC GGT GCT GGC TTT GTG CTG GGC CTG GTG GAT ATC ATC     192
495   Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
496            50                 55                  60
497
498   TGG GGC ATT TTT GGT CCC TCC CAA TGG GAC GCC TTT CTG GTG CAA ATT     240
499   Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
500    65                 70                  75                  80
501
502   GAA CAG CTG ATT AAC CAA CGC ATC GAA GAA TTC GCT AGG AAC CAA GCC     288
503   Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
504                85                 90                  95
505
506   ATT TCC CGC CTG GAA GGC CTG AGC AAT CTG TAC CAA ATT TAC GCC GAA     336
507   Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
508            100                105                 110
509
510   TCC TTT CGC GAG TGG GAA GCC GAT CCT ACC AAT CCA GCC CTG CGC GAA     384
```

```
511    Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
512        115             120             125
513
514    GAG ATG CGC ATT CAA TTC AAT GAC ATG AAC AGC GCC CTG ACC ACC GCT    432
515    Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
516        130             135             140
517
518    ATT CCT CTG TTT GCC GTG CAA AAT TAC CAA GTG CCT CTG CTG TCC GTG    480
519    Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
520    145             150             155             160
521
522    TAC GTG CAA GCT GCC AAT CTG CAT CTG TCC GTG CTG CGC GAT GTG TCC    528
523    Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
524            165             170             175
525
526    GTG TTT GGC CAA AGG TGG GGC TTT GAT GCC GCC ACC ATC AAT AGC CGC    576
527    Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
528            180             185             190
529
530    TAC AAT GAT CTG ACC AGG CTG ATT GGC AAC TAC ACC GAT TAC GCT GTG    624
531    Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
532            195             200             205
533
534    CGC TGG TAC AAT ACC GGC CTG GAA CGC GTG TGG GGC CCA GAT TCC CGC    672
535    Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
536        210             215             220
537
538    GAT TGG GTG AGG TAC AAT CAA TTT CGC CGC GAA CTG ACC CTG ACC GTG    720
539    Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
540    225             230             235             240
541
542    CTC GAT ATC GTG GCT CTG TTC CCA AAT TAC GAT AGC CGC CGC TAC CCA    768
543    Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
544            245             250             255
545
546    ATT CGA ACC GTG TCC CAA CTG ACC CGC GAA ATT TAC ACC AAC CCA GTG    816
547    Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
548            260             265             270
549
550    CTG GAA AAT TTT GAT GGT AGC TTT CGC GGC TCC GCT CAG GGC ATC GAA    864
551    Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
552        275             280             285
553
554    CGC AGC ATT AGG AGC CCA CAT CTG ATG GAT ATC CTG AAC AGC ATC ACC    912
555    Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
556        290             295             300
557
558    ATC TAC ACC GAT GCT CAT AGG GGT TAC TAC TAC TGG TCC GGC CAT CAA    960
559    Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
560    305             310             315             320
561
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562   ATC ATG GCT TCC CCT GTG GGC TTT TCC GGG CCA GAA TTC ACC TTT CCA      1008
563   Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
564               325             330                 335

565
566   CTG TAC GGC ACG ATG GGC AAT GCC GCT CCA CAA CAA CGC ATT GTG GCT      1056
567   Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
568               340             345                 350

569
570   CAA CTG GGT CAG GGC GTG TAC CGC ACC CTG TCC TCC ACC CTG TAC CGC      1104
571   Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
572               355             360                 365

573
574   CGC CCT TTT AAT ATC GGC ATC AAC AAC CAG CAA CTG TCC GTG CTG GAC      1152
575   Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
576               370             375                 380

577
578   GGC ACC GAA TTT GCT TAC GGC ACC TCC TCC AAT CTG CCA TCC GCT GTA      1200
579   Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
580   385             390                 395                 400

581
582   TAC CGC AAG AGC GGC ACC GTG GAT TCC CTG GAT GAA ATC CCA CCA CAG      1248
583   Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
584               405             410                 415

585
586   AAT AAC AAC GTG CCA CCT AGG CAA GGC TTT AGC CAT CGC CTG AGC CAT      1296
587   Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
588               420             425                 430

589
590   GTG TCC ATG TTT CGC TCC GGC TTT AGC AAT AGC AGC GTG AGC ATC ATC      1344
591   Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
592               435             440                 445

593
594   CGC GCT CCT ATG TTC TCC TGG ATC CAC CGC TCC GCT GAG TTC AAC AAC      1392
595   Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
596   450             455                 460

597
598   ATC ATC CCG TCC TCC CAA ATC ACC CAA ATC CCG CTC ACC AAG TCC ACG      1440
599   Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
600   465             470                 475                 480

601
602   AAC CTC GGC TCC GGC ACG TCC GTC GTC AAG GGC CCG GGC TTC ACC GGC      1488
603   Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
604               485             490                 495

605
606   GGC GAC ATC CTC CGC CGC ACG TCC CCG GGC CAG ATC TCC ACC CTC CGC      1536
607   Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
608               500             505                 510

609
610   GTC AAC ATC ACG GCT CCG CTG AGC CAG CGC TAC AGG GTG CGC ATC AGA      1584
611   Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
612               515             520                 525
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

DATE: 09/07/93
TIME: 15:22:26

INPUT SET: S1444.raw

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613
614    TAC GCT AGC ACG ACC AAC CTG CAA TTC CAC ACG TCC ATC GAC GGC AGA      1632
615    Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
616        530                 535                 540
617
618    CCG ATC AAC CAG GGC AAC TTC AGC GCG ACG ATG AGC TCC GGG TCC AAC      1680
619    Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
620    545                 550                 555                 560
621
622    CTC CAG TCC GGC TCC TTC CGC ACG GTC GGT TTC ACC ACG CCG TTC AAC      1728
623    Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
624                565                 570                 575
625
626    TTC TCC AAC GGC TCC TCC GTC TTC ACG CTC TCC GCT CAC GTC TTC AAC      1776
627    Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
628                580                 585                 590
629
630    TCC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTC CCG GCC GAG      1824
631    Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
632                595                 600                 605
633
634    GTC ACC TTC GAG CTC GAG TAGGTA                                      1848
635    Val Thr Phe Glu Leu Glu
636        610
637
638
639    (2) INFORMATION FOR SEQ ID NO:13:
640
641            (i) SEQUENCE CHARACTERISTICS:
642                (A) LENGTH: 614 amino acids
643                (B) TYPE: amino acid
644                (D) TOPOLOGY: linear
645
646            (ii) MOLECULE TYPE: protein
647
648            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
649
650    Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
651     1               5                  10                  15
652
653    Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
654                20                  25                  30
655
656    Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
657     .          35                  40                  45
658
659    Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
660            50                  55                  60
661
662    Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
663     65                  70                  75                  80
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/113,561*

DATE: 09/07/93
TIME: 15:22:33

INPUT SET: S1444.raw

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664
665     Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
666                     85                      90                  95
667
668     Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
669                 100                     105                 110
670
671     Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
672             115                     120                 125
673
674     Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
675         130                     135                 140
676
677     Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
678     145                     150                 155                 160
679
680     Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
681                     165                     170                 175
682
683     Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
684                 180                     185                 190
685
686     Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
687             195                     200                 205
688
689     Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
690         210                     215                 220
691
692     Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
693     225                     230                 235                 240
694
695     Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
696                 245                     250                 255
697
698     Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
699             260                     265                 270
700
701     Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
702             275                     280                 285
703
704     Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
705         290                     295                 300
706
707     Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
708     305                     310                 315                 320
709
710     Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
711                 325                     330                 335
712
713     Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
714             340                     345                 350
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715
716    Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
717        355             360             365
718
719    Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
720        370             375             380
721
722    Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
723    385             390             395             400
724
725    Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
726            405             410             415
727
728    Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
729            420             425             430
730
731    Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
732        435             440             445
733
734    Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
735        450             455             460
736
737    Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
738    465             470             475             480
739
740    Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
741            485             490             495
742
743    Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
744            500             505             510
745
746    Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
747        515             520             525
748
749    Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
750        530             535             540
751
752    Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
753    545             550             555             560
754
755    Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
756            565             570             575
757
758    Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
759            580             585             590
760
761    Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
762            595             600             605
763
764    Val Thr Phe Glu Leu Glu
765        610
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/113,561*

DATE: 09/07/93
TIME: 15:22:46

INPUT SET: S1444.raw

766
767

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/113,561*

INPUT SET: S1444.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: unknown
29	Wrong Filing Date	(B) FILING DATE: August 25, 1993
30	Wrong Classification	(C) CLASSIFICATION: unknown

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/08/113,561*

INPUT SET: S1444.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/08/113,561*

INPUT SET: S1444.raw

Line	Original Text	Corrected Text
5	(i) APPLICANTS: Adams, Thomas R. et al.	(i) APPLICANT: Adams, Thomas R. et al.